

1. (Three Times Amended) A method of determining a consensus profile for a first plurality of perturbations to a cell type or organism, said method comprising identifying [common response motifs] among a plurality of sets of cellular constituents in a plurality of response profiles one or more sets of cellular constituents, each of said one or more sets of cellular constituents being upregulated or downregulated by said first plurality of perturbations, each response profile in said plurality of response profiles (i) comprising measurements of a plurality of cellular constituents, and (ii) resulting from a different perturbation to said type of cell or organism, wherein each [of said sets] set of cellular constituents in said plurality of sets of cellular constituents consists of cellular constituents that co-vary under a second plurality of perturbations or that are co-regulated, wherein said plurality of response profiles comprises at least five response profiles, and wherein said [common response motifs constitute the] consensus profile for said first plurality of perturbations comprises measurements of said one or more sets of cellular constituents.

3. (Amended) The method of claim [2] 1, wherein the plurality of response profiles comprises more than ten response profiles.

6. (Twice Amended) The method of claim 1, wherein [the] said first plurality of perturbations are associated with a particular biological effect.

19. (Amended) The method of claim 1, wherein the [common response motifs] one or more sets of cellular constituents are identified by re-ordering the response profiles into sets associated with similar biological effects.

29. (Twice Amended) A method of determining a consensus profile for a first plurality of perturbations to a cell type or organism, said method comprising identifying [common response motifs] among a plurality of sets of cellular constituents in a plurality of projected profiles one or more sets of cellular constituents, each of said one or more sets of cellular constituents being upregulated or downregulated by said first plurality of perturbations, each projected profile in said plurality of projected profiles

(i) resulting from a different perturbation to said type of cell or organism, and

(ii) comprising measurements of a plurality of cellular constituents in said type of cell or organism that have been projected onto basis cellular constituent sets, said basis cellular constituent sets being defined by co-variation of measurements of cellular constituents under a second plurality of different perturbations, wherein said [common response motifs constitute the] consensus profile for said first plurality of perturbations comprises projected measurements of said one or more sets of cellular constituents.

30. (Twice Amended) The method of claim 1 wherein the consensus profile is the intersection of the sets of cellular constituents activated or de-activated [in the common response motifs] by said first plurality of perturbations.

31. (Twice Amended) The method of claim 29, wherein the consensus profile is the intersection of the sets of cellular constituents activated or de-activated [on the common response motifs] by said first plurality of perturbations.

32. (Amended) The method of claim 30 or 31, wherein the [common response motifs] one or more sets of cellular constituents are identified by re-ordering the response profiles into sets associated with similar biological effects.

38. (Three times Amended) A method of determining a consensus profile for a first plurality of perturbations to a cell type or organism, said method comprising identifying [common response motifs] among a plurality of sets of genes in a plurality of response profiles one or more sets of genes, each of said one or more sets of genes being upregulated or downregulated by said first plurality of perturbations, each response profile in said plurality of response profiles (i) comprising measurements of transcript levels for a plurality of genes, and (ii) resulting from a different perturbation to said type of cell or organism, wherein each [of said sets] set of genes in said plurality of sets of genes consists of genes having transcripts that co-vary under a second plurality of perturbations or that are co-regulated, and wherein said [common response motifs constitute the] consensus profile for said perturbations comprises measurements of transcript levels for said one or more sets of genes.

39. (Twice Amended) A method for comparing a biological response profile to a consensus profile, said consensus profile comprising [common response motifs among a plurality of projected response profiles] projected measurements of one or more sets of cellular constituents, said one or more sets having been identified among a plurality of sets of cellular constituents in a plurality of projected response profiles, each of said one or more sets of cellular constituents being upregulated or downregulated by a first plurality of perturbations, each projected response profile in said plurality of projected response profiles

(i) resulting from a different perturbation to said type of cell or organism, and
(ii) comprising measurements of a plurality of cellular constituents in said type of cell or organism that have been projected onto basis cellular constituent sets, said basis cellular constituent sets being defined by co-variation of measurements of cellular constituents under a second plurality of different perturbations, [wherein said common response motifs constitute the consensus profile for said of perturbations,] said method comprising:

- (a) converting the biological response profile into a projected response profile by projecting measurements of cellular constituents in said biological response profile onto said basis cellular constituent sets; and
- (b) determining the value of a similarity metric between the projected response profile and the consensus profile.

44. (Three Times Amended) A method for grouping measured response profiles in sets which are associated with similar biological effects comprising grouping response profiles [into sets] among a plurality of response profiles into sets, each of said sets of response profiles consisting of response profiles in which the responses of one or more sets of cellular constituents in each response profile are similar among response profiles in the set, each response profile in said plurality of response profiles (i) comprising measurements of a plurality of cellular constituents, and (ii) resulting from a different perturbation, wherein each of said sets of cellular constituents consists of cellular constituents that co-vary under a plurality of perturbations or that are co-regulated, wherein said plurality of response profiles comprises at least five response profiles.

72. (Twice Amended) A method for analyzing response data from a biological sample comprising

- (a) grouping cellular constituents from the biological sample into sets of cellular constituents that co-vary in a plurality of response profiles, each response profile in said plurality of response profiles (i) comprising measurements of a plurality of cellular constituents, and (ii) resulting from a different perturbation to said biological sample; and
- (b) grouping the plurality of response profiles into sets of response profiles that similarly affect cellular constituents,

wherein said plurality of response profiles comprises at least five response profiles.

100. (Twice Amended) A method of grouping sets of perturbations that similarly affect cellular constituents in a cell type or organism among a plurality of perturbations comprising grouping response profiles among a plurality of response profiles in sets, each of said sets of response profiles consisting of response profiles in which the responses of one or more sets of cellular constituents are similar among the response profiles in the set, each response profile in said plurality of response profiles (i) comprising measurements of a plurality of cellular constituents, and (ii) resulting from a different perturbation, wherein each of said sets of cellular constituents consists of cellular constituents that co-vary under a plurality of perturbations or that are co-regulated, thereby grouping said sets of perturbations, wherein said plurality of response profiles comprises at least five response profiles.

REMARKS

Claims 1-50, 58-64, 72-78, and 89-106 were pending in the application. In the instant Amendment, claim 2 has been canceled without prejudice and claims 1, 3, 6, 19, 29-32, 38-39, 44, 72 and 100 have been amended to more particularly point out and distinctly claim the present invention. Upon entry of the above-made amendments, claims 1, 3-50, 58-64, 72-78, and 89-106 will be pending. A marked version showing changes made to the amended claims is attached hereto as Exhibit A. A clean version of the pending claims, as amended, is attached hereto as Exhibit B.

Claim 1 has been amended to more particularly point out that the claimed method is for determining a consensus profile for a first plurality of perturbations by identifying *one or more sets of cellular constituents, each of said one or more sets of cellular constituents being upregulated or downregulated by said first plurality of perturbations* and that the consensus